

OM of: us-09-743-492-1 to: PIR_68:* out_format : pfs

Date: May 13, 2002 9:45 AM

About: Results were produced by the GenCore software, version 4.5,
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Command line parameters: -DRV=slp

-MODEL=framed-n2p.model
-Q/cgml2_1/USPTO_spool/US09743492/runat_13052002_093834_19627/app_query.fasta_1.3580
-DB=PIR_68 -QPMF=fastan -SUFFIX=tr -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOPEXT=0.000 -OGAPOP=4.500
-OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-DELEXT=7.000 -XGAPOP=10.000 -XGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=50 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=20 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
-MAXLEN=200000000 -USER=US09743492 -CGNL_1_269 -NCPU=6 -ICPU=3
-LONGLOG -NO_XLPXY -WAIT -THREADS=1

Search information block:

Query: US-09-743-492-1

Query length: 3467

Database: PIR_68*

Database sequences: 219241

Database length: 76174552

Search time (sec): 161.560000

score_list:

Sequence	Strd	Orig	ZScore	EScore	Len	Documentation
PIR1:TDHULK	+	3236.00	3838.56	4.2e-207	1897	! leukocyte antigen-related protein
PIR2:AS6493	+	3176.50	3771.13	3.6e-203	1290	! leukocyte common antigen-related protein
PIR2:AS4216	+	3172.00	3762.20	7.6e-203	1898	! leukocyte antigen-related protein
PIR2:AS7068	+	3057.00	3635.89	2.7e-195	582	! protein-tyrosine-phosphatase (EC 2.7.1.1)
PIR2:AS6178	+	2926.00	3468.63	1.7e-186	1912	! protein-tyrosine-phosphatase (EC 2.7.1.1)
PIR1:DS4689	+	2874.50	3408.32	4.4e-183	1691	! protein-tyrosine-phosphatase (EC 2.7.1.1)
PIR2:CS4689	+	2874.50	3407.27	4.5e-183	1894	! protein-tyrosine-phosphatase (EC 2.7.1.1)
PIR2:IS0212	+	2867.50	3401.08	4.3e-182	1499	! protein-tyrosine-phosphatase (EC 2.7.1.1)
PIR2:IS8148	+	2850.00	3380.18	1.8e-181	1501	! protein-tyrosine-phosphatase (EC 2.7.1.1)
PIR2:IS0893	+	2847.00	3374.40	3.0e-181	1907	! protein-tyrosine-phosphatase (EC 2.7.1.1)
PIR2:SA6217	+	2844.00	3371.03	4.8e-181	1863	! protein-tyrosine-phosphatase (EC 2.7.1.1)
PIR1:AA8758	+	2753.50	3265.08	4.7e-175	1496	! protein-tyrosine-phosphatase (EC 2.7.1.1)
PIR2:SS3089	+	2509.00	2975.17	8.1e-159	1231	! protein-tyrosine-phosphatase (EC 2.7.1.1)
PIR1:TDPELK	+	2503.00	2963.40	2.2e-158	2029	! protein-tyrosine-phosphatase (EC 2.7.1.1)
PIR2:TS1093	+	2450.50	2903.95	6.4e-155	1437	! probable protein-tyrosine-phosphatase (EC 2.7.1.1)
PIR2:IS6540	+	2377.00	2812.97	5.2e-150	2051	! receptor tyrosine phosphatase (EC 2.7.1.1)
PIR1:TD1921	+	1836.50	2170.48	4.2e-114	1585	! probable protein-tyrosine-phosphatase (EC 2.7.1.1)
PIR2:AS3605	+	1551.00	1836.14	3.4e-95	802	! protein-tyrosine-phosphatase (EC 2.7.1.1)
PIR1:BA8758	+	1538.00	1816.45	2.7e-94	1262	! protein-tyrosine-phosphatase (EC 2.7.1.1)
PIR1:JC1285	+	1525.00	1805.19	1.8e-93	796	! protein-tyrosine-phosphatase (EC 2.7.1.1)
PIR1:AA7373	+	1518.00	1796.46	5.4e-93	829	! protein-tyrosine-phosphatase (EC 2.7.1.1)
PIR1:SI2053	+	1429.00	1691.83	4.3e-87	700	! protein-tyrosine-phosphatase (EC 2.7.1.1)
PIR2:JC6132	+	1423.00	1684.69	1.1e-86	699	! protein-tyrosine-phosphatase (EC 2.7.1.1)
PIR1:SI1670	+	1307.00	1539.55	6.3e-79	1452	! protein-tyrosine-phosphatase (EC 2.7.1.1)
PIR1:SI1769	+	1306.00	1538.36	7.3e-79	1452	! protein-tyrosine-phosphatase (EC 2.7.1.1)
PIR1:AA8066	+	1243.00	1463.16	1.1e-74	1440	! protein-tyrosine-phosphatase (EC 2.7.1.1)
PIR2:JC6312	+	1236.00	1454.92	3.3e-74	1440	! protein-tyrosine-phosphatase (EC 2.7.1.1)
PIR1:AA8148	+	1168.00	1373.75	1.1e-69	1445	! protein-tyrosine-phosphatase (EC 2.7.1.1)
PIR2:JC5290	+	1166.50	1372.02	1.4e-69	1436	! protein-tyrosine-phosphatase (EC 2.7.1.1)
PIR1:BA8148	+	1162.00	1366.61	2.7e-69	1442	! protein-tyrosine-phosphatase (EC 2.7.1.1)
PIR2:TA42636	+	1142.00	1342.88	5.8e-68	1422	! protein-tyrosine-phosphatase (EC 2.7.1.1)
PIR2:IS72441	+	1135.50	1335.00	1.6e-67	1442	! protein-tyrosine-phosphatase (EC 2.7.1.1)
PIR1:AA6151	+	1117.50	1309.16	2.7e-66	2314	! protein-tyrosine-phosphatase (EC 2.7.1.1)
PIR1:AA11622	+	1089.50	1281.06	1.8e-64	1301	! protein-tyrosine-phosphatase (EC 2.7.1.1)
PIR2:AS4080	+	1048.50	1232.61	9.2e-62	1237	! protein-tyrosine-phosphatase (EC 2.7.1.1)
PIR1:TDPELT	+	1038.00	1219.82	4.6e-61	1273	! leukocyte common antigen precursor
PIR1:AA6546	+	1035.50	1216.62	6.8e-61	1304	! leukocyte common antigen long
PIR1:AA28334	+	1017.00	1194.64	1.2e-59	1291	! protein-tyrosine-phosphatase (EC 2.7.1.1)
PIR2:TA3148	+	1013.00	1190.54	2.1e-59	1200	! probable protein-tyrosine-phosphatase (EC 2.7.1.1)
PIR1:B36182	+	1011.50	1186.93	2.7e-59	1462	! protein-tyrosine-phosphatase (EC 2.7.1.1)

PIR2:TA42522	+	894.00	1047.08	1.8e-51	1409	! protein-tyrosine-phosphatase
PIR2:TS0111	+	876.50	1026.12	2.6e-50	1422	! hypothetical protein F56D1.1
PIR1:AS5148	+	702.00	816.21	1.0e-38	1711	! protein-tyrosine-phosphatase
PIR2:AA0169	+	697.00	827.77	1.6e-38	256	! protein-tyrosine-phosphatase
PIR2:TS2738	+	635.00	744.37	2.5e-34	711	! hypothetical protein T13H5.1
PIR2:TS2308	+	634.50	739.30	3.0e-34	1156	! hypothetical protein K04D7.1
PIR2:T14328	+	631.00	728.77	5.8e-34	2302	! protein-tyrosine-phosphatase
PIR1:AA9724	+	625.00	728.27	1.3e-33	1118	! protein-tyrosine-phosphatase
PIR2:AA9502	+	611.50	707.94	1.1e-32	1767	! protein-tyrosine-phosphatase

seq_name: pirl:TDHULK

seq_documentation_block:

leukocyte antigen-related protein precursor - human

N:Alternate names: leukocyte common antigen homolog

N:Contains: protein-tyrosine-phosphatase (EC 3.1.3.48)

C:Species: Homo sapiens (man)

C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 22-Jun-1999

C:Accession: S03841; J10051

R:Streuli, M.; Krueger, N.X.; Hall, L.R.; Schlossman, S.F.; Saito, H.

J. Exp. Med. 168, 1523-1530, 1988

A:Title: A new member of the immunoglobulin superfamily that has a cytoplasmic region

A:Reference number: J10051; MUID:89035978

A:Accession: S03841

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-1897 <STR>

A:Cross-references: EMBL:Y00815; NID:934266; PIDN:CAA68754.1; PID:934267

C:Genetics:

A:Gene: GDB:PTPRF; LAR

A:Cross-references: GDB:L20138; OMIM:179590

A:Map position: lp34-lp34

C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homolog

C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane

F:1-16/Domain: signal sequence #status predicted <SIG>

F:17-1897/Product: leukocyte antigen-related protein #status predicted <MAT>

F:17-1250/Domain: extracellular #status predicted <EXT>

F:37-99/Domain: immunoglobulin homology <IMM1>

F:139-199/Domain: immunoglobulin homology <IMM2>

F:236-290/Domain: immunoglobulin homology <IMM3>

F:308-390/Domain: fibronectin type III repeat homology <FN3A>

F:403-489/Domain: fibronectin type III repeat homology <FN3B>

F:501-583/Domain: fibronectin type III repeat homology <FN3C>

F:596-685/Domain: fibronectin type III repeat homology <FN3D>

F:698-798/Domain: fibronectin type III repeat homology <FN3E>

F:810-893/Domain: fibronectin type III repeat homology <FN3F>

F:905-989/Domain: fibronectin type III repeat homology <FN3G>

F:1001-1078/Domain: fibronectin type III repeat homology <FN3H>

F:1251-1274/Domain: transmembrane #status predicted <TM>

F:1275-1897/Domain: intracellular #status predicted <INT>

F:1285-1897/Domain: leukocyte common antigen cytosolic domain homology <LAC>

F:1365-1586/Domain: protein-tyrosine-phosphatase homology <PTP1>

F:1654-1877/Domain: protein-tyrosine-phosphatase homology <PTP2>

F:44-97, 146-197, 243-288/Disulfide bonds: #status predicted

F:107, 240, 285, 711, 956/Binding site: carbohydrate (asn) (covalent) #status predicted

F:1538/Active site: Cys (phosphocysteine intermediate) #status predicted

F:1544/Binding site: substrate phosphate (Arg) #status predicted

F:1829/Active site: Cys (phosphocysteine intermediate) #status predicted

F:1835/Binding site: substrate phosphate (Arg) #status predicted

alignment_scores:

Quality: 3236.00 Length: 607

Ratio: 5.331 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-743-492-1 x TDHULK

Align seg 1/1 to: TDHULK from: 1 to: 1897

6 GGACTGAAGGACTCCTTCTGCTGGCCCACTCCTCTGACCCCTGTGGAGATGCG 55

1291 GlyLeuLysAspSerLeuLeuAlaHisSerSerAspProValGluMetAr 1307
56 GAGCTCAACTACAGACCCAGAGTATGCGAGACCCACCCACCCATCCCA 105
1307 GArGLuAsnTyRGlnThrProGlyMetArgSpHisProProlleProI 1324
106 TCACCGACCTGGGGGCAACATCGAGCGCTCAAAGCCAACGATGGCCTC 155
1324 leThrAspLeuAlaAspAsnIleGluArgLeuLysAlaAsnAspGlyLeu 1340
156 AGTTCTCCAGAGATGATGATCCATCGACCGCTGGAGCAGAGTTCAGTG 205
1341 LysPheSerGlnGluTyRGluSerIleAspProGlyGlnGlnPheThrTr 1357
206 GGAGAAATCAACCTGGAGTGAACAGCCCAAGACCCGCTATCCGATG 255
1357 pGluAsnSerAsnLeuGluValAsnLysProLysAsnArgTyRAlaAsnV 1374
256 TCATCGCCTACGACCACTCTCGAGTCACTCTTACCTCTATCGATGGC 305
1374 alIleAlaTyRAspHisSerArgValIleLeuThrSerIleAspGlyVal 1390
306 CCGGGAGTCACTACATCAATGCCAATGATCGATGGCTACCGCAAGCA 355
1391 ProGlySerAspTyRileAsnAlaAsnTyRileAspGlyTyRArgLysGI 1407
356 GAATGCTTACATCCCAACGAGCGGCCCTTGCAGACCATGGCGGATT 405
1407 nAsnAlaTyRileAlaThrGlnGlyProLeuProGluThrMetGlyAspP 1424
406 TCTGGAGAATGGTGGGAACAGCGCACGGCCACTGTGTTCATGATGACA 455
1424 heTrpArgMetValTrpGluGluArgThrAlaThrValValMetMetThr 1440
456 CGCTGGAGAGAGTCCCGGGTAAATGTGATCAGTACTGCGCCAGCCCG 505
1441 ArgLeuGluGlnLysSerArgValLysCysAspGlnTyRtrpProAlaAr 1457
506 TGGCACCAGACCTGTGGCTTATTAGGTGACCCCTGTTGGACACAGTGG 555
1457 gGlyThrGluThrCysGlyLeuIleGlnValThrLeuLeuAspThrValG 1474
556 AGCTGGCCACATACATGTGCGCACCTTCCACTCCACAGAGTGGCTCC 605
1474 luLeuAlaThrTyRThrValArgThrPheAlaLeuHisLysSerGlySer 1490
606 AGTGAGAAGCGTCAGCTGGCTCAGTTTCAGTTTCATGCTGCGCCAGACCA 655
1491 SerGlyLysArgGluLeuArgGlnPheGlnPheMetAlaTrpProAspHI 1507
656 TGGAGTTCCTGAGTACCCAACTCCCATCCTGGCTTCTCCTACGACGGTCA 705
1507 sGlyValProGluTyRProThrProlleLeuAlaPheLeuArgArgValL 1524
706 AGCCCTGCACCCCTAGACGAGGCGCCATGTGTGTGCTACTCCACGGCG 755
1524 ysAlaCysAsnProLeuAspAlaGlyProMetValValHisCysSerAla 1540
756 GCGTGGCGCGCACCGCTGCTTCATCGTGATGATGCCATGTGGAGCG 805
1541 GlyValGlyArgThrGlyCysPheIleValIleAspAlaMetLeuGluAr 1557
806 GATGAAGCAGCAGAGACGGTGACATCTATGGCCACGCTGACCTGCATGC 855
1557 gMetLysHisGluLysThrValAspIleTyRGlyHisValThrCysMeta 1574
856 GATCAGAGGAACACTACATGGTGCAGAGGAGGACCATGATGTTTCATC 905
1574 rgSerGlnArgAsnTyRMetValGlnThrGluAspGlnTyRValPheIle 1590
906 CATGAGGCGCTGCTGGAGGCTGCCAGTGGCGCCACACAGAGTGGCTGC 955

1591 HisGluAlaLeuLeuGluAlaAlaThrCysGlyHisThrGluValProAl 1607
956 CCCAACCTGTATGCCACATCCAGAGCTGGCCCAAGTCCCTCCAGGGG 1005
1607 aArgAsnLeutyRAlaHisIleGlnLysLeuGlyGlnValProProGlyG 1624
1006 AGAGTGTGACCGCATGGAGTTCAGTTCAAGTTGCTGGCCAGCTCCAAG 1055
1624 luserValThrAlaMetGluLeuGluPheLysLeuLeuAlaSerSerLys 1640
1056 GCCCACAGTCCCGCTTCATCAGCGCCAACTGCCCTGCAACAGTTCAA 1105
1641 AlaHisThrSerArgPheIleSerAlaAsnLeuProCysAsnLysPheLy 1657
1106 GAACCGCTGGTGAACATCATGCCCTACGAATTCACCCGTGTGTCTGTC 1155
1657 sAsnArgLeuValAsnIleMetProTyRGluLeuThrArgValCysLeuG 1674
1156 AGCCCATCCGTGTGTGGAGGCTCTGACTACATCAATGCCAGCTTCCTG 1205
1674 lnProIleArgGlyValGluGlySerAspTyRileAsnAlaSerPheLeu 1690
1206 GATGGTTATAGACAGCAGAGGCTTACATAGCTACAGAGGCTCTGGC 1255
1691 AspGlyTyRArgGlnGlnLysAlaTyRileAlaThrGlnGlyProLeuAl 1707
1256 AGAGACACCGAGGACTTCTGGCGCATGCTATGGAGCACAATTCACCA 1305
1707 aGluSerThrGluAspPheTrpArgMetLeuTrpGluHisAsnSerThrI 1724
1306 TCATCGTCAATGTGACCAAGCTTCGGGAGATGGGAGGAGAGAAATGCCAC 1355
1724 leIleValMetLeuThrLysLeuArgGluMetGlyArgGluLysCysHis 1740
1356 CAGTACTGCGCAGCAGCGCTCTGCTCGCTACAGTACTTCTGTTGA 1405
1741 GlnTyRtrpProAlaGluArgSerAlaArgTyRGlnTyRtrpPheValValAs 1757
1406 CCGATGGTGTGATACAACATGCCAGTATATCCTCGCTGAGTTCAAGG 1455
1757 pProMetAlaGluTyRAsnMetProGlnTyRileLeuArgGluPheLysV 1774
1456 TCACGGATCCCGGGATGGGACGTCAAGACAATCCGGCAGTTCAGTTC 1505
1774 alThrAspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPhe 1790
1506 ACAGACTGCGCAGCAGCGCTGCCCAAGACAGCAGCGGAGGATTCATTGA 1555
1791 ThrAspTrpProGluGlnGlyValProLysThrGlyGlyGlyPheIleAs 1807
1556 CTTTCATCGGCGCAGGTGCATAAGACCAAGAGCAGTTCGGACAGATGGGC 1605
1807 pPheIleGlyGlnValHisLysThrLysGluGlnPheGlyGlnAspGlyP 1824
1606 CTTATCAGGTGCTACTGCTGCTGGCGTGGCGCCGACCCGGGTGTTTCATC 1655
1824 roIleThrValHisCysSerAlaGlyValGlyArgThrGlyValPheIle 1840
1656 ACPTCTCAGCATGCTCTGGAGCGCATGCGCTATGAGGCGCTGCTGCACAT 1705
1841 ThrLeuSerIleValLeuGluArgMetArgTyRGlyGlyValValaspme 1857
1706 GTTTCAGACCGTGAAGACCTCGTGTACACAGCGTCTCTGCGATGGTGCAGA 1755
1857 tPheGlnThrValLysThrLeuArgThrGlnArgProAlaMetValGlnT 1874
1756 CAGAGACCATGATCATGCTGCTACCGTGGCGCCCTCGAGTACCTGGCC 1805
1874 hrGluAspGlnTyRGlnLeuCysTyRArgAlaAlaLeuGluTyRLeuGly 1890
1806 AGCTTTGACCACTATGCAACG 1826
1891 SerPheAspHisTyRAlaThr 1897

seq_name: pir2:A56493

seq_documentation_block:

leucocyte common antigen-related protein (LAR) - rat (fragment)

N:Alternate names: LAR receptor-linked tyrosine phosphatase

N:Contains: protein-tyrosine-phosphatase (EC 3.1.3.48)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000

C:Accession: A56493; 155393

R:Zhang, J.S.; Longo, F.M.

J. Cell Biol. 128, 415-431, 1995

A:Title: LAR tyrosine phosphatase receptor: alternative splicing is preferential to the

A:Reference number: A56493; MUID:95146548

A:Accession: A56493

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1290 <RES>

A:Cross-references: EMBL:X83505; NID:g732918; PIDN:CAA58495.1; PID:g732919

P:Longo, F.M.; Martignetti, J.A.; Le Beau, J.M.; Zhang, J.S.; Barnes, J.P.; Brosius, J.

Biol. Chem. 268, 26503-26511, 1993

● Title: Leukocyte common antigen-related receptor-linked tyrosine phosphatase. Regulati

A:Reference number: 155393; MUID:94075340

A:Accession: 155393

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 831-1290 <RE2>

A:Cross-references: EMBL:U00477; NID:g392565; PIDN:AAC04306.1; PID:g392566

C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;

ogy

C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatas

F:80-166/Domain: fibronectin type III repeat homology <3FR>

F:667-1290/Domain: leukocyte common antigen cytosolic domain homology <LAC>

F:1047-1270/Domain: protein-tyrosine-phosphatase homology <PIR2>

F:931/Active site: Cys (phosphotyrosine intermediate) #status predicted

F:937/Binding site: substrate phosphate (Arg) #status predicted

F:1222/Active site: Cys (phosphotyrosine intermediate) #status predicted

F:1228/Binding site: substrate phosphate (Arg) #status predicted

alignment_scores:

Quality: 3176.50 Length: 618

Ratio: 5.268 Gaps: 1

Percent Similarity: 97.573 Percent Identity: 96.926

alignment_block:

US-09-743-492-1 x A56493 ..

align seg 1/1 to: A56493 from: 1 to: 1290

6 GCAGTCAAGGACTCTGCTGCGCCACTCTCTGACCCCTGTGGAGATGCG 55

673 GlyLeuLysAspSerLeuLeuAlaHisSerSerAspProValGluMetAr 689

56 GAGGCTCAACTACACACCCAGGT..... 80

689 gArgLeuAsnTyrGlnThrProGlySerSerAlaProSerCysProAsnI 706

81ATCGGAGACCAACCCATCCCATCCAGCCTGGCGGAC 122

706 leSerSerMetArgAspHisProProIleProIleThrAspLeuAlaAsp 722

123 ACATCGAGCGCCTCAAGCCCAACGATGCGCTCAAGTCTCCAGAGTA 172

723 AsnIleGluArgLeuLysAlaAsnAspGlyLeuLysPheSerGlnGluTyr 739

173 TCAGTCCATCGACCTGGACACAGTTCACGTGGGAGATTCAAACCTGG 222

739 rGluSerIleAspProGlyGlnGlnPheThrIrpGluAsnSerAsnSerg 756

223 AGGTGAACCAAGCCCAAGAACCGCTATCGGAATCTCATCGCTTACGACCA 272

756 luValAsnLysProLysAsnArgTyrAlaAsnValIleAlaTyrAspHis 772

273 TCTCGAGTCACTCTTACCTCTATCGATGCGGTCCTCCCGGGAGTCACTACAT 322

773 SerArgValLeuLeuThrSerIleAspGlyValProGlySerAspTyrIl 789

323 CAATGCCAACTACATCGATGGCTACCGCAAGCAGAGATGCTTACATCGCCA 372

789 eAsnAlaAsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyrIleAlaT 806

373 CGCAGGGCCCTGCGCCGAGACCATGGCGATTCTCGAGAAATGGTGTGG 422

806 hrGlnGlyProLeuProGluThrMetGlyAspPheTrpArgMetValTrp 822

423 GAACAGCGCACGCCCACTGCTGTCATGATGACACGCTGGAGGAGAAGTC 472

823 GluGlnArgThrAlaThrValValMetMetThrArgLeuGluGluLysSe 839

473 CGGGTAAATGTGATCAGTACTGGCCAGCCGCTGGCACCAGAGACCTGTG 522

839 rArgValLysCysAspGlnTyrTrpProAlaArgGlyThrGluThrTyrG 856

523 GCCTATTTCAGGTGACCCCTGTGGACACAGTGGAGCTGGCCACATACACT 572

856 lylLeuIleGlnValThrLeuValAspThrValGluLeuAlaThrTyrThr 872

573 GTGCGCACCTTCGCACCTCCACAGAGTGGCTCCAGTGAGAAGCGTGAGCT 622

873 MetArgThrPheAlaLeuHisLysSerGlySerSerGluLysArgGluLe 889

623 GGCTCAGTTTTCAGTTTCATGGCTGGCCAGACCATGGAGTTCCTGAGTACC 672

889 uArgGlnPheGlnPheMetAlaTrpProAspHisGlyValProGluTyrP 906

673 CAACTCCCATCTGCGCTCTTACAGACGGGTCAAGCCCTGCAACCCCTTA 722

906 roThrProIleLeuAlaPheLeuArgArgValLysAlaCysAsnProLeu 922

723 GACGAGGCGCCATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 772

923 AspAlaGlyProMetValValHisCysSerAlaGlyValGlyArgThrGl 939

773 CTGCTTCATCGTATTGATGCCATGTTGGAGCGGATGAAGCAGCAGAGA 822

939 yCysPheIleValIleAspAlaMetLeuGluArgMetLysHisGluLys 956

823 CGGTGGACATCTATGCCACGCTGACCTGATGCGATCAGAGGAACACTAC 872

956 hrValAspIleTyrGlyHisValThrCysMetArgSerGlnArgAsnTyr 972

873 ATGGTGCAGACGAGGACACAGTACGTGTTTCATCCATGAGCGCTGCTGGA 922

973 MetValGlnThrGluAspGlnTyrValPheIleHisGluAlaLeuLeuGl 989

923 GGCTGCGCAGCTGCGGCCACACAGAGGTGCTGCGCCCAACCTGTATGCC 972

989 uAlaAlaMetCysGlyHisThrGluValLeuAlaArgAsnLeuTyrAlaH 1006

973 ACATCCAGAGCTGGGCCCAAGTGCCTCCAGGGGAGAGTGTGACCGCCATG 1022

1006 lsIleGlnLysLeuGlyGlnValProProGlyGluSerValThrAlaMet 1022

1023 GAGCTCGAGTTTCAAGTTGCTGGCCAGCTCCAAGGCCACACGTCCTCCG 1072

1023 GluLeuGluPheLysLeuLeuAlaAsnSerLysAlaHisThrSerArgPh 1039

1073 CATCAGCGCAACCTGCTGCTGCAACAAGTTCAGAAACCCGCTGGTGAACA 1122

1039 eIleSerAlaAsnLeuProCysAsnLysPheLysAsnArgLeuValAsnI 1056

1123 TCATGCCCTTACGAATGTACCCGCTGTGTGTCTGACGCCCATCCGCTGTG 1172

1056 leMetProTyrGluLeuThrArgValCysLeuGlnProIleArgGlyVal 1072

1173 GAGGGCTGCTGACTACATCAATGCCAGCTTCTCTGGATGGTTATAGACAGCA 1222
 |||||
 1073 GluclySerAspTyrIleAsnAlaSerPheLeuAspGlyTyrArgGlnG1 1089
 |||||
 1223 GAGGGCTGCTGACTACATCAATGCCAGCTTCTCTGGATGGTTATAGACAGCA 1272
 |||||
 1089 nLysAlaTyrIleAlaThrGlnGlyProLeuAlaGluSerThrGluAsp 1106
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seq_documentation_block:

leukocyte antigen-related protein precursor - rat

N:Alternate names: leukocyte common antigen homolog

N:Contains: protein-tyrosine-phosphatase (EC 3.1.3.48)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #text_change 23-Jul-1999

C:Accession: S46216; S23252; A41032; A33154

B:Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.

Biochem. J. 302, 39-47, 1994

A:Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-ph

A:Reference number: S46216; MUID:94347119

A:Accession: S46216

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-1898 <ZHA>

A:Cross-references: EMBL:LI1586; NID:g205132; PIDN:AAC37655.1; PID:g205133
 B:Hashimoto, N.; Zhang, W.R.; Goldstein, B.J.
 Biochem. J. 284, 569-576, 1992
 A:Title: Insulin receptor and epidermal growth factor receptor dephosphorylation by t
 A:Reference number: S23126; MUID:92287069
 A:Accession: S23252
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1361-1604; 1649-1898 <HAS>
 R:Pot, D.A.; Woodford, T.A.; Remboutsika, E.; Haun, R.S.; Dixon, J.E.
 J. Biol. Chem. 266, 19688-19696, 1991
 A:Title: Cloning, bacterial expression, purification, and characterization of the cyt
 A:Reference number: A41032; MUID:92011772
 A:Accession: A41032
 A:Molecule type: mRNA
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 A:Cross-references: GB:M60103; NID:g205130; PIDN:AAA41510.1; PID:g205131
 R:Pot, D.A.; Woodford, T.A.; Remboutsika, E.; Haun, R.S.; Dixon, J.E.
 Submitted to the Protein Sequence Database, December 1990
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 C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homolog
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 C:Keywords: duplication; glycoprotein; phosphoprotein; phosphoric monoester hydrolase
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 F:149-209/Domain: immunoglobulin homology <IMM2>
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 F:413-499/Domain: fibronectin type III repeat homology <FN3B>
 F:511-593/Domain: fibronectin type III repeat homology <FN3C>
 F:606-695/Domain: fibronectin type III repeat homology <FN3D>
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 F:1545/Binding site: substrate phosphate (Arg) #status predicted
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C;Date: 03-Oct-1995 #sequence_revision 09-Mar-1996 #text_change 23-Jul-1999

C:Accession: A57068; S40280
 R:Schaapveld, R.Q.J.; van den Maagdenberg, A.M.J.M.; Schepens, J.T.G.; Olde Weghuis, D.;
 Genomics 27, 124-130, 1995
 A:Title: The mouse gene ptpfr encoding the leukocyte common antigen-related molecule LAR
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 R:Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
 submitted to the EMBL Data Library, June 1993
 A:Description: Assessment of the expression levels of murine protein-tyrosine phosphatases
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 A:Accession: S40280
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 C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane
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N:protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta, splice form D precu
N:Alternate names: WPTP delta type D
N:Contains: protein tyrosine phosphatase, receptor type delta, splice form A
C:Species: Mus musculus (house mouse)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: D54689; A54689
R:Mizuno, K.; Hasegawa, K.; Katagiri, T.; Ogimoto, M.; Ichikawa, T.; Yakura, H.
Mol. Cell. Biol. 13, 5513-5523, 1993
A:Title: WPTP delta, a putative murine homolog of HPTP delta, is expressed in special
A:Reference number: A54689; MUID:93360986
A:Accession: D54689
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1691 <MI2>
A:Experimental source: brain
A>Note: sequence inconsistent with nucleotide translation
A>Note: sequence extracted from NCBI backbone (NCBIN:137486, NCBI:P:136537)
A:Accession: A54689
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-398,799-1691 <MI2>
A:Experimental source: brain
A>Note: sequence inconsistent with nucleotide translation
A>Note: sequence extracted from NCBI backbone (NCBIN:136522, NCBI:P:136524)
C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology
og
C:Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester
F;42-95/Domain: immunoglobulin homology <IMM3>
F;114-196/Domain: fibronectin type III repeat homology <FN3A>
F;1075-1691/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F;1449-1671/Domain: protein-tyrosine-phosphatase homology <ppp2>
F;1333/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1339/Binding site: substrate phosphate (Arg) #status predicted
F;1623/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1629/Binding site: substrate phosphate (Arg) #status predicted

alignment_scores:
Quality: 2874.50 Length: 599
Ratio: 4.956 Gaps: 3
Percent Similarity: 96.828 Percent identity: 89.149

alignment_block:

US-09-743-492-1 x D54689

Align seg 1/1 to: D54689 from: 1 to: 1691

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30  CACTCTCTGACCCCTGTGAGATGGGAGGCTCAACTACCAGACCCAGG 79
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1096 HisProThrAspProValGluLeuArgLeuAsnPheGlnThrProG 1112
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
80  TATGGAGACCCACCACCATCCCATCCAGCTGGCGGACAAACATCG 129
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1112 yMetAlaSerHisProPheProIleLeuGluLeuAlaAspHisIleG 1129
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
130  AGCGCTCAAGCAACGATGCCTCAAGTTCTCCAGGAGTATGATGCC 179
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1129 luArgLeuLysAlaAsnAspAsnLeuLysPheSerGlnGluTyrGluSer 1145
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
180  ATCGACCTCGGACAGAGTTACGTGGGAGAATTCAACCTCGAGGTGAA 229
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1146 IleAspProGlyGlnGlnPheThrTrpGluHisSerAsnLeuGluValAs 1162
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
230  CAAGCCCAAGACCGCTATGCGAATGTCATCGCTACGACCACTCTCGAG 279
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1162 nLysProLysAsnArgTyrAlaAsnValIleAlaTyrAspHisSerArgV 1179
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
280  TCATCCTTACCTCTATCGATGGCGTCCCGGGAGTGACTACATCATGCC 329
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1179 aLeuLeuSerAlaIleGluGlyIleProGlySerAspTyrValAsnAla 1195
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
330  AACTACATCATCGGTGTACCGCAAGCAGAGATGCTACATCCCGCAGCGG 379
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1196 AsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyrIleAlaThrGlnG 1212
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
380  CCCCTGCCGAGACATGGCGGATTTCTGGAGATGTTGGTGGGAACAGC 429
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1212 ySerLeuProGluThrPheGlyAspPheTrpArgMetIleTrpGluGlnG 1229
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
430  GCACGGCCACTGTGTCATGATGACACGGCTGGAGGAGAGTCCCGGTA 479
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1229 lu...AlaThrValMetMetThrLysLeuGluGluArgSerArgVal 1244
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
480  AATGTGTACGTACTGTGGCCAGCCGTGGCAGCAGACCTGTGGCTTAT 529
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1245 LysCysAspGlnTyrTrpProSerArgGlyThrGluThrHisGlyLeuVa 1261
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
530  TCAGGTGACCCCTGTGGACACAGTGGAGCTGGCCACATACACTGTGGCG 579
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1261 lGlnValThrLeuLeuAspThrValGluLeu...ThrTyrCysValArgT 1277
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
580  CCTTCGCACTCCACACAGTGGCTCCAGTGAGAAGCGTGAGTGGGTGAG 629
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1277 hrPheAlaLeuTyrAsnAsnGlySerSerGluLysArgLysValArgGln 1293
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
630  TTTTCAGTTTCATGGCTGGCCAGACCATGAGTTCTCTAGTACCCCAACTCC 679
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1294 PheGlnPheThrAlaTrpProAspHisGlyValProGluHisProThrPr 1310
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
680  CATCTGCGCTTCTTCAGACGGGTCAAGCCCTGCAACCCCTAGACGCAG 729
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1310 oPheLeuAlaPheLeuArgArgValLysThrCysAsnProProAspAlaG 1327
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
730  GCGCCATGGTGTGCTACTGCACGGCGGGGTGGCGGCACCGCTGCTTC 779
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1327 lypProMetValValHisCysSerAlaGlyValGlyArgThrGlyCysPhe 1343
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
780  ATCTGATTGATGATGCTGTGAGCGGATGAAGCACGAGAACCGGTGGA 829
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1344 lIleValIleAspAlaMetLeuGluArgIleLysHisGluLysThrValAs 1360
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
830  CATCTATGGCCACGTGACCTGCATCGCATCAGAGGAACACTACATGGTGC 879
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1360 pIleTyrGlyHisValThrLeuMetArgAlaGlnArgAsnTyrMetValG 1377
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```
880  AGACGGAGGACCACTACGTGTTTCATCTCCATGAGCGCTGCTGGAGGCTGCC 929
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1377 lInThrGluAspGlnTyrIlePheIleHisAspAlaLeuLeuGluAlaVal 1393
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
930  AGCTGGCGCACACAGAGGTGCTGCCCGCAACCTGTATGCCACCATCCA 979
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1394 ThrCysGlyAsnThrGluValProAlaArgAsnLeuTyrAlaTyrIleG 1410
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
980  GAAGCTGGGCCAAGTGCCTCCAGGGGAGAGTGTGACCCCATGGAGCTCG 1029
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1410 nLysLeuThrGlnIleGluThrGlyGluAsnValThrGlyMetGluLeuG 1427
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1030 AGTTCAAGTTGCTGGCCAGCTCCAGGCCCCACAGCTCCCGCTTCATCAGC 1079
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1427 lUpheLysArgLeuAlaSerSerLysAlaHisThrSerArgPheIleSer 1443
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1080 GCCAAGCTGCTGCAACCAAGTTCAAGAACCCGCTGCTGAACATCATGCC 1129
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1444 AlaAsnLeuProCysAsnLysPheLysAsnArgLeuValAsnIleMetPr 1460
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1130 CTACGAATTGACCCGTGTGTCTGCAGCCCATCCGTGTGTGGAGGGCT 1179
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1460 oTyrGluSerGlyArgValCysLeuGlnProIleArgGlyValGluGlyS 1477
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1477 eAspTyrIleAsnAlaSerPheLeuAspGlyTyrArgGlnGlnLysAla 1493
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
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1280 CATGCTATGGGAGACCAATTCACCATCATGCTGCTGACCAACATGCC 1329
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1330 GGGAGATGGCAGGAGAAATGCCACAGTACTGGCCAGCAGAGCGCTCT 1379
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1527 rGluMetGlyArgGluLysCysHisGlnTyrTrpProAlaGluArgSer 1543
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1480 CAAGGACAAATCCGGCAGTTCACAGTTCACAGTGGCCAGAGAGCGCGTG 1529
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1576 eArgThrValArgGlnPheGlnPheThrAspTrpProGluGlnGlyVal 1592
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1593 ProLysSerGlyGluGlyPheIleAspPheIleGlyGlnValHisLysTh 1609
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1580 CAAGGACAGTGTGGACAGGATGGGCTATCATCGGTGCTGCTGAGTGTG 1629
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1609 rLysGluGlnPheGlyGlnAspGlyProIleSerValHisCysSerAlaG 1626
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1630 GGTGGGCGCCACCGGGGTGTTTCATCCTGAGCATCGTCTGGAGCGC 1679
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1626 lYvalGlyArgThrGlyValPheIleThrLeuSerIleValLeuGluArg 1642
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1680 ATCGCTATGAGGGGTGCTGCACATGTTTTCAGACCGTGAAGACCCCTGCC 1729
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1643 MetArgTyrGluGlyValValAspIlePheGlnThrValLysMetLeuAr 1659
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1730 TACACAGCGTCTGCCATGGTCCACAGAGGACCATCATGCTAGCTGTGCT 1779
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1659 gThrGlnArgProAlaMetValGlnThrGluAspGlnTyrGlnPheCyst 1676
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1780 ACCGTGCGCCCTGGAGTACCTGCGGAGCTTGCACCACTATGCAACG 1826
|||||
1676 yArgAlaAlaLeuGluTyrLeuGlySerPheAspHisTyrAlaThr 1691

seq_name: pir2:C54689

seq_documentation_block:
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta, splice form B precursor
N:Alternate names: MPTP delta type B/C
C:Contains: protein tyrosine phosphatase, receptor type delta, splice form C
C:Species: Mus musculus (house mouse)
C:Date: 25-Apr-1995 #sequence_revision 19-May-1995 #text_change 12-Feb-1999
C:Accession: C54689; B54689
R:Mizuno, K.; Hasegawa, K.; Katagiri, T.; Ogimoto, M.; Ichikawa, T.; Yakura, H.
Mol. Cell. Biol. 13, 5513-5523, 1993
A:Title: MPTP delta, a putative murine homolog of HPTP delta, is expressed in specialized
A:Reference number: A54689; MUID:93360986
A:Accession: C54689
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1894 <MTZ>
A:Experimental source: brain; splice form B
A:Note: sequence inconsistent with nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:137486, NCBIP:137487)
A:Accession: B54689
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-352, 'H', 354-535, 'S', 537-601, 1002-1894 <MT2>
A:Experimental source: brain; splice form C
A:Note: sequence inconsistent with nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:136527, NCBIP:136530)
C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
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C:Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hyd
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F:245-299/Domain: immunoglobulin homology <IMM2>
F:317-399/Domain: fibronectin type III repeat homology <FN3A>
F:1278-1894/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F:1652-1874/Domain: protein-tyrosine-phosphatase homology <PTP2>
F:1536/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1542/Binding site: Cys (phosphocysteine intermediate) #status predicted
F:1826/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1832/Binding site: substrate phosphate (Arg) #status predicted

alignment_scores:

Quality: 2874.50 Length: 599
Ratio: 4.956 Gaps: 3
Percent Similarity: 96.828 Percent Identity: 89.149

alignment_block:

US-09-743-492-1 x C54689

Align seg 1/1 to: C54689 from: 1 to: 1894

30 CACTCCTCTGACCCCTGTGGAGATGGGGAGCTCAACTACGACCCGAGG 79
||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1299 HisProThrAspProValGluLeuArgArgLeuAsnPheGlnThrProG 1315
80 FATGGAGACACCCACCCATCCCATCCAGCTACCCAGCTGGGGGACACATCG 129
||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1315 yMetAlaSerHisProPheGlnProLeuGluLeuAlaAspHisIleG 1332
130 AGCGCTCAAGCCCAACGATGGCTCAAGTCTCCAGGAGTATGATGCC 179
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180 ATCGACCCCTGGACAGCTTCAAGTGGGAGAAATCAACCTGGAGGTGAA 229
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1349 IleAspProGlyGlnGlnPheThrTrpGluHisSerAsnLeuGluValAs 1365
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1365 nLysProLysAsnArgTyrAlaAsnValIleAlaTyrAspHisSerArgV 1382
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630 TTTTCACTTCCCTGGCGGACAGCATGAGTTCCTGAGTACCAACTCC 679
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1647 AlaAsnLeuProCysAsnLysPheLysAsnArgLeuValAsnIleMetPr 1663
1130 CTACGAATGTACCGTGTGTCTCGACGCCCATCCGTGGTGGAGGGCT 1179
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1663 oTyrGluSerGlyArgValCysLeuGlnProIleArgGlyValGluGlys 1680

1180 CTGACTACATCAATGCCAGCTCTCCGGATGTTATAGACAGACAGAGGCC 1229
|||||
1680 erasprryrlleasnalaSerPheLeuAspGlyTyrArgGlnGlnysAla 1696
|||||
1230 TACATAGCTACACAGGGGCTCTGGCAGAGACACCGAGGACTTCTGGCG 1279
|||||
1697 TyrIleAlaThrGlnGlyProLeuAlaGluThrGluAspPheTrpAr 1713
|||||
1280 CATGCTATGGGAGACAAATTCACCATCATCGTCATGTCGACCAAGCTTC 1329
|||||
1713 gMetLeuTrpGluHisAsnSerThrIleValValMetLeuThrLysLeuA 1730
|||||
1330 GGGAGATGGCAGGAGAGAAATGCCACGACTCTGGCCAGCAGCGCTCT 1379
|||||
1730 rgLumetGlyArgGluLysCysHisGlnTyrTrpProAlaGluArgSer 1746
|||||
1380 GTCGCTACCACTACTTGTGTTGACCCGATGGCTGAGTACAAATGCC 1429
|||||
1747 AlaArgTyrGlnTyrPheValValAspProMetAlaGluTyrAsnMetPr 1763
|||||
1430 CCAGTATATCTCGCTGAGTCAAGGTCAAGTCCAGGATCCCGGGATGGCAGT 1479
|||||
1763 oGlnTyrIleLeuArgGluPheLysValThrAspAlaArgAsp...Glns 1779
|||||
1480 CAAGACAAATCCGGCAGTTCACAGTTCACAGACTGGCCAGCAGGCGCTG 1529
|||||
1779 erArgThrValArgGlnPheGlnPheThrAspTrpProGluGlnGlyVal 1795
|||||
1530 CCCAAGACAGGCGAGGATTCATTCATCTCCGGCAGGTCATCAAGAC 1579
|||||
1796 ProLysSerGlyGluGlyPheIleAspPheIleGlyGlnValHisLysTh 1812
|||||
1580 CAAGGACGAGTTGGACAGGATGGCCATCAGCGTGCAGTGCAGTGGTG 1629
|||||
1812 rLysGluGlnPheGlyGlnAspGlyProIleSerValHisCysSerAlaG 1829
|||||
1630 GCGTGGCGCCACCGGGGTTCATCTCAGTCTGAGCATCGTCTGGAGCGC 1679
|||||
1829 lyValGlyArgThrGlyValPheIleThrLeuSerIleValLeuGluArg 1845
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1680 ATGCGCTATGAGGGCGTGTGCACATGTTTCAGACCGTGAAGACCCCTGG 1729
|||||
1846 MetArgTyrGluGlyValValAspIlePheGlnThrValLysMetLeuAr 1862
|||||
1730 TACACAGCGTCTCGCATGGTCCACAGAGACGACCATCATCAGTGTGCT 1779
|||||
1862 gThrGlnArgProAlaMetValGlnThrGluAspGlnTyrGlnPheCysT 1879
|||||
1780 ACCGTGGCGCCCTGGAGTACCTCGGCGAGCTTGGACCATATGCAACG 1826
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1879 yrArgAlaAlaLeuGluTyrLeuGlySerPheAspHisTyrAlaThr 1894
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seq_name: pir2: I50212

seq_documentation_block:

protein-tyrosine-phosphatase (EC 3.1.3.48) - chicken

C:Species: Gallus gallus (chicken)

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jan-2000

C:Accession: I50212

R:Stoker, A.W.

Mech. Dev. 46, 201-217, 1994

A:Title: Isoforms of a novel cell adhesion molecule-like protein tyrosine phosphatase ar

A:Reference number: I50212; MUID:95001563

A:Accession: I50212

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1499 <STO>

A:Cross-references: GB:L32780; NID:g485746; PIDN:AAA64460.1; PID:g485747

C:Genetics:

A:Gene: CRYPalpal

C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;

ogy

C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
P:148-208/Domain: immunoglobulin homology <IMM1>
F:245-299/Domain: immunoglobulin homology <IMM2>
F:317-399/Domain: fibronectin type III repeat homology <3PR>
F:881-1479/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F:1257-1479/Domain: protein-tyrosine-phosphatase homology <PMP2>
F:1141/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1147/Binding site: substrate phosphate (Arg) #status predicted
F:1432/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1438/Binding site: substrate phosphate (Arg) #status predicted

alignment_scores:

Quality: 2867.50 Length: 599

Ratio: 4.944

Percent Similarity: 96.828 Percent Identity: 87.980

alignment_block:

US-09-743-492-1 x I50212

Align seg 1/1 to: I50212 from: 1 to: 1499

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902 HisProLysAspProValGluMetArgGileAsnPheGlnThrProGl 918
|||
80 TATCGAGACACCCACCATCCCATCACCGCTGGGGGACACATCG 129
|||
918 yMetLeuSerHisProIleProValSerGluLeuAlaGluHisThrG 935
|||
130 ACGCCTCAAGCCCAACGATGGCTCAAGTCTCCAGGAGTATGATGCC 179
|||
935 LuHisLeuLysAlaAsnAspAsnLeuLysLeuSerGlnGluTyrGluSer 951
|||
180 ATCGACCTGGACAGCTTCACGTGGGAGAAATCAACCTGGAGGTGAA 229
|||
952 IleAspProGlyGlnGlnPheThrTyrGluHisSerAsnLeuGluValAs 968
|||
230 CAAGCCCGAGAACCGCTATCGCAATGTCTATCGCTACGACCTCTCGAG 279
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968 nLysProLysAsnArgTyrAlaAsnValIleAlaTyrAspHisSerArgv 985
|||
280 TCATCCTTTACCTCTATCGATGGCTGGCGGAGTCTCCAGGAGTATGATGCC 329
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985 alileLeuLeuProIleGluGlyIleValGlySerAspTyrIleAsnAla 1001
|||
330 AACTCATCGATGGCTACCGCAAGCAGAAATGCCTACATCGCCACCGAGG 379
|||
1002 AsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyrIleAlaThrGlnGl 1018
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380 CCCCCTGGCCGAGACCATGGCGATTTCTGGAGAAATGGTGTGGGAACAGC 429
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1018 yProLeuProGluThrPheGlyAspPheTrpArgMetValTrpGluGlnA 1035
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430 GCACGGCCACTGTGTCTATGATGACACGCTGGAGGAGAGTCCCGGTA 479
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1035 rgSerAlaThrIleValMetMetThrLysLeuGluGluLysSerArgIle 1051
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480 AAATGTGATGATCTAGTGGCCAGCCCGTGGCACCAGACCTGTGGCTTAT 529
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1052 LysCysAspGlnTyrTrpProGlyArgGlyThrAspThrTyrGlyMetIl 1068
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530 TCAGTGGACCTGTGGACACAGTGGAGCTGGCCACATACACTGTGCCGA 579
|||
1068 eGlnValThrLeuLeuAspThrIleGluLeuAlaThrPheCysValArgt 1085
|||
580 CCTCGCACTCCACAAGAGTGGCTCCAGTGAAGCGTGAAGCTGCCTCAG 629
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1085 hrPheSerLeuHisLysAsnGlySerSerGluLysArgGluValArgGln 1101
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630 TTTCAGTTTCATGGCTGGCCGACCATGGAGTTCCTGAGTACCCCACTCC 679
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1102 PheGlnPheThrAlaTrpProAspHisGlyValProGluTyrProThrPr 1118
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680 CATCTGGCTTCCTACGAGGTCAGGCTCAAGCCCTGCAACCCCTAGACGCAG 729
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1118 oPheLeuAlaPheLeuArgArgValLysThrCysAsnProProAspAlaG 1135
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730 GGCCCATGTGTGCTACTACGACGGGGGGCTGGCGCCACCGCTCTTC 779
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1135 lyProileValValHisCysSerAlaGlyValGlyArgThrGlyCysPhe 1151
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780 ATCGTGATTCATCCATGTGTGAGCGGATGAAGCAGCAGAACGGTGA 829
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1152 IleValIleAspAlaMetLeuGluArgIleLysHisGluLysThrValAs 1168
|||||
830 CATCTATGCCACGTGACCTGCATCGGATCACAGAGGAACACTACATGCTC 879
|||||
1168 pIleTyrglyHisValThrLeuMetArgSerGlnArgAsnTyrmelValG 1185
|||||
880 AGACGGAGACCATGACGTGTTTCATCCATGAGCGGCTGCTGGAGGCTGCC 929
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1185 InThrGluAspGlnTyrsPheIleHisAspAlaLeuLeuGluAlaVal 1201
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930 AGTGGGGCCACACAGAGTGTGCTGCCGCCACCTGTATGCCACATCCA 979
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1202 AlaCysGlyAsnThrGluValProAlaArgAsnLeuTyThrTyrIleG 1218
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980 GAAGCTGGGGCCAAAGTGCCTCCAGGGAGAGTGTGACCGCATGGAGCTCG 1029
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1218 nLysLeuAlaGlnIleGluValGlyGluHisValThrGlyMetGluLeuG 1235
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1030 AGTTCAAGTTGCTGGCCACTCCTCAAGGCCACACGTCCTCGCTTCATCAGC 1079
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1235 luPheLysArgLeuAlaAsnSerLysAlaHisThrSerArgPheIleSer 1251
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1080 GCCAAGCTCCCTGCAACAGTTCAGAACCGCTGCTGAACATATGCC 1129
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1252 AlaAsnLeuProCysAsnLysPheLysAsnArgLeuValAsnIleMetPr 1268
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1130 CTACGAATTCACCGCTGTGTCTGCGAGCCCATCCGTGTGTGGAGGGCT 1179
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1268 oTyrgluThrArgValCysLeuGlnProIleArgGlyValGluGlyS 1285
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1180 CTGACTACATCAATGCCAGCTTCCTGGATGGTATAGACAGCAGAGGCC 1229
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1285 eAspTyrlleAsnAlaSerPheIleAspGlyTyArgGlnGlnLysAla 1301
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1230 TCATAGCTACACAGGGGCTCTGGCAGAGACCGAGGACTTCTGGCG 1279
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1302 TyrlleAlaThrGlnGlyProLeuAlaGluThrThrGluAspPheTrpAr 1318
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1280 CATGCTATGGGAGCACAAATTCACCATCATCTGCTGACCAAGCTTC 1329
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1318 gMetLeuTrpGluAsnAsnSerThrIleValValMetLeuThrLysLeuA 1335
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1330 GGGAGATGGGAGGAGAAATGCCACCATCTGCTGCGCAGCAGAGCGCTCT 1379
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1335 rgGluMetGlyArgGluLysCysHisGlnTyTrpProAlaGluArgSer 1351
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1380 GCTCGCTACCACTACTTGTGTCACCGATGGCTGAGTACAAATGCC 1429
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1352 AlaArgTyrgluTyPheValValAspProMetAlaGluTyAsnMetPr 1368
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1430 CCAGTATATTCCTCGGTGAGTTCAGAGTCCAGGATGCCGGGATGGGCAGT 1479
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1368 oGlnTyrlleLeuArgGluPheLysValThrAspAlaArgAspGlyGlnS 1385
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1480 CAAGACAAATCCGGGATTCACATTCACAGACTGCCAGAGCAGGCGTG 1529
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1385 eArgThrValArgGlnPheGlnPheThrAspTrpProGluGlnGlyVal 1401
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1468 gThrGln...ProAlaMetValGlnThrGluAspGluTyrglnPheCysT 1484
|||||
1780 ACCGTGGCGCCCTGGAGTACCTCGCGAGCTTTGACCACTATGCAAGC 1826
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1484 yrGlnAlaAlaLeuGluTyrgluLeuGlySerPheAspHisTyrlaThr 1499
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seq_name: pir2:I58148

seq_documentation_block:

protein-tyrosine-phosphatase (EC 3.1.3.48) 2B, splice form LAR - rat
N:Alternate names: leukocyte common antigen-related phosphatase
C:Species: Rattus norvegicus (Norway rat)

C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 20-Jun-2000

C:Accession: I58148; S46218

R:Walton, K.M.; Martell, K.J.; Kwak, S.P.; Dixon, J.E.; Largent, B.L.
Neuron 11, 387-400, 1993

A:Title: A novel receptor-type protein tyrosine phosphatase is expressed during neuro

A:Reference number: I58148; MUID:93357030

A:Accession: I58148

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-1501 <WAL>

A:Cross-references: GB:L19933; NID:g310242; PIDN:AAA42309.1; PID:g310243

A:Note: in Genbank entry RATTYRPHOS, release 113.0, the source is designated as Rattu

R:Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.

Biochem. J. 302, 39-47, 1994

A:Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-

A:Reference number: S46218; MUID:94347119

A:Accession: S46218

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-1501 <ZHA>

A:Cross-references: EMBL:L12329; NID:g294573; PIDN:AAC37657.1; PID:g294574

C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homolog

ogy

C:Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; tyr

F:47-109/Domain: immunoglobulin homology <IMM1>

F:149-209/Domain: immunoglobulin homology <IMM2>

F:246-300/Domain: immunoglobulin homology <IMM3>

F:413-506/Domain: fibronectin type III repeat homology <3FR>

F:882-1501/Domain: leukocyte common antigen cytosolic domain homology <LAC>

F:969-1190/Domain: protein-tyrosine-phosphatase homology <PTP1>

F:1258-1481/Domain: protein-tyrosine-phosphatase homology <PTP2>

F:1142/Active site: Cys (phosphocysteine intermediate) #link PTP1 #status predicted

F:1148/Binding site: substrate phosphate (Arg) #link PTP1 #status predicted

F:1433/Active site: Cys (phosphocysteine intermediate) #link PTP2 #status predicted

F:1439/Binding site: substrate phosphate (Arg) #link PTP2 #status predicted

alignment_scores:

Quality: 2850.00 Length: 599

Ratio: 4.914 Gaps: 0

Percent Similarity: 96.828 Percent Identity: 87.312

alignment_block:

US-09-743-492-1 x I58148

Align seg 1/1 to: I58148 from: 1 to: 1501

seq_documentation_block:

protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type sigma precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C:Accession: S50893; S40281
R:Wagner, J.; Boerboom, D.; Tremblay, M.L.
Eur. J. Biochem. 226, 773-782, 1994
A:Title: Molecular cloning and tissue-specific RNA processing of a murine receptor-type
A:Reference number: S50893; MUID:95112841
A:Accession: S50893
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-1907 <WAG>
A:Cross-references: EMBL:X82288; NID:g587483; PIDN:CAA57732.1; PID:g587484
R:Henriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
submitted to the EMBL Data Library, June 1993
A:Description: Assessment of the expression levels of murine protein-tyrosine phosphatase
A:Reference number: S40280
A:Accession: S40281
A:Molecule type: mRNA
A:Residues: 1441-1501, 'E', 1503-1546 <HEN>
A:Cross-references: EMBL:223050; NID:g438137; PIDN:CAA80585.1; PID:g438138
C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
cay

C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane
F:149-209/Domain: immunoglobulin homology <IMM1>
F:246-300/Domain: immunoglobulin homology <IMM2>
F:413-506/Domain: fibronectin type III repeat homology <3PR>
F:1288-1507/Domain: leukocyte common antigen cytosolic domain homology <PTP1>
F:1375-1596/Domain: protein-tyrosine-phosphatase homology <PTP2>
F:1684-1887/Domain: protein-tyrosine-phosphatase homology <PTP2>
F:1548/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1554/Binding site: substrate phosphate (Arg) #status predicted
F:1839/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1845/Binding site: substrate phosphate (Arg) #status predicted

alignment_scores:

Quality: 2847.00 Length: 599
Ratio: 4.909 Gaps: 0
Percent Similarity: 96.828 Percent Identity: 87.145

alignment_block:

US-09-743-492-1 x S50893

Align seq 1/1 to: S50893 from: 1 to: 1907

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30  CACTCTCTGACCTGTGGAGATGCGGAGCTCACTACCAGCCAGG 79
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1309 HisProLysAspProValGluMetArgArgIleAsnPhcGlnThrProG1 1325

80  TATGCGAGACCCACCCATCCCAATCCAGCTGCGGCGGCAACATCG 129
    |||  ::|||::|||::|||::|||::|||::|||::|||::|||
1325 yMetLeuSerHisProProllethrAspMetAlaGluHisMetG 1342

130  AGCGCTCAAGCCAAACAGATGGCTCAAGTCTCCAGGAGTATGATCC 179
    |||  ::|||::|||::|||::|||::|||::|||::|||::|||
1342 LuArgLeuLysAlaAsnAspSerLeuLysLeuSerGlnGluTyGluSer 1358

180  ATCGACCTGGACAGAGTTCAGTGGGAGAAATCAACCTGAGGTGAA 229
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1359 IleAspProGlyGlnPheThrTrpGluHisSerAsnLeuGluAlaAs 1375

230  CAAGCCCAAGAACCGCTATGCGAATGCTACGCTACGACCACTCTCGAG 279
    |||  ::|||::|||::|||::|||::|||::|||::|||::|||
1375 nLysProLysAsnArgTyAlaAsnValIleAlaTyAspHisSerArgV 1392

280  TCATCCTTACCTCTATCGATGGCGTCCCGGGAGTGACTACATCAATGCC 329
    |||  ::|||::|||::|||::|||::|||::|||::|||::|||
1392 alIleLeuGlnProLeuGluGlyIleMetGlySerAspTyIleAsnAla 1408

330  AACTACATCATGGCTACCGCAGCAGAGATGCTACATGCCACGAGGG 379
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1425 yProLeuProGluThrPheGlyAspPheTrpArgMetValTrpGluGlnA 1442

430  GCACGGCCACTGTGGTCATCATCACACGGCTGGAGGAGAAAGTCCCGGGA 479
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1442 rGserAlaThrValValMetMetThrArgLeuGluGluLysSerArgIle 1458

480  AAATGTATCAGTACTGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTAT 529
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580  CCTTCGACCTCCACAAAGAGTGGCTCCAGTGAGAAAGGTGAGTGCCTGAG 629
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1492 hrPheSerLeuHisLysAsnGlySerSerGlyLysArgGluValArgHis 1508

630  TTTCAGTTCATGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTCC 679
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1509 PheGlnPheThrAlaTrpProAspHisGlyValProGluTyTrpThrPr 1525

680  CATCTGGCGCTTCTCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 729
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1525 oPheLeuAlaPheLeuArgArgValLysThrCysAsnProProAspAlaG 1542

730  GGCCCTAGTGTGTGCACTGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCTTC 779
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1542 lyProIleValValHisCysSerAlaGlyValGlyArgThrGlyCysPhe 1558

780  ATCGTATGATGCCATCTGTGGAGCGGATGCAACGACGAGAGAGCGGTGGA 829
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1592 lnThrGluAspGlnTyGlyPheIleHisGluAlaLeuLeuGluAlaVal 1608

930  ACCTGGCGGCGCACACAGAGTGCCTGCCCGGCGGCGGCGGCGGCGGCGGCG 979
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980  GAAGCTGGGCGCAAGTGCCTCCAGGCGGAGAGTGTGACCGCGCATGGAGCTCG 1029
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1625 nLysLeuAlaGlnValGluProGlyGluHisValThrGlyMetGluLeuG 1642

1030  AGTTCAGTGTGTGGCGAGCTCCAGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1079
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1642 LuPheLysArgLeuAlaSerSerLysAlaHisThrSerArgPheIleThr 1658

1080  GCCAACTGCCCTGCCAAACAGTTCACAGACCGGCTGGTGCACATCATGCC 1129
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1130  CTACGAATTCACCCGTGTGTCTGCGAGCGGCGGCGGCGGCGGCGGCGGCGT 1179
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1180  CTGACTACATCAATGCCAGCTTCTCTGGATGGTGTATAGACAGCAGAAAGGCC 1229
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1230  TACATAGCTACACAGGCGGCTCTGGCAGAGAGACCGAGAGCTTCTGGCG 1279
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1709 TyIleAlaThrGlnGlyProLeuAlaGluThrThrGluAspPheTrpAr 1725
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730 GGCCCATGGTGTGCTGACTGACGCGGGGGGGGGCCGCGCCAGCGCTCTTC 779
|||||
1498 lyProValValValHisCysSerAlaGlyValGlyArgThrGlyCysPhe 1514
|||||
780 ATCGTGATTGATGCCATGTTGGAGCGGATGAAGCAGCAGAACGCGTGA 829
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1515 lleValileasPalaMetLeuGluArgIleArgThrGluLysThrValAs 1531
|||||
830 CATCTATGCGCCACGTGACCTGCATCGATCAGAGAGAACTACATGGTGC 879
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1531 pValTyGlyHisValThrLeuMetArgSerGlnArgAsnTyMetValIG 1548
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880 AGACGAGGACACAGTACGTGTTTCATCCATGAGGCGCTGCTGAGGCTGCC 929
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1548 lnThrGluAspGlnTySerPheIleHisGluAlaLeuLeuGluAlaVal 1564
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930 ACGTGCGGCCACACAGAGTGTCTGCCCAACCTGTATGCCACATCCA 979
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1030 AGTTCAAGTTGCTGGCAGCTCCAGGCCACACGTCCTCCGCTTCATCAGC 1079
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1598 luPheLysArgLeuAlaSerSerLysAlaHisThrSerArgPheIleThr 1614
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1080 GCCAAGTTCCTCCCAAGTTCAGAACCGCTGCTGAACATCATGCC 1129
|||||
1615 AlaSerLeuProCysAsnLysPheLysAsnArgLeuValAsnIleLeuPr 1631
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1130 CTACGAATTGACCCGTGTGTGTCTGTCAGCCCATCCGTGTGTGGGGCT 1179
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1631 oTyrgLuserSerArgValCysLeuGlnProIleArgGlyValGluGlyS 1648
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1180 CTGACTACATCAATGCCAGCTTCCTGGATGGTTATAGACAGAGAGGCC 1229
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1648 exAspTyrrileAsnAlaSerPheIleAspGlyTyArgGlnGlnLysAla 1664
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1230 TACATAGCTACACAGGGGCTCTGSCAGAGCACCAGGAGCTCTGGCG 1279
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1665 TyrrileAlaThrGlnGlyProLeuAlaGluThrThrGluAspPheTrpAr 1681
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1280 CATGTATGGGAGCAATTCACCATCATCTGCTGCTGACCAAGCTTC 1329
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1681 gAlaLeuTrpGluAsnAsnSerThrIleValValMetLeuThrLysLeuA 1698
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1330 GGGAGATGGGAGGAGAAATCCACCACTACTGCGCCAGCAGAGCGCTCT 1379
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1698 rgGluMetGlyArgGluLysCysHisGlnTyTrpProAlaGluArgSer 1714
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1380 GCTCGCTACCACTACTTGTCTTCCCGGATGGCTGAGTACAACTGCC 1429
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1715 AlaArgTyrgLntyrPheValValAspProMetAlaGluTyAsnMetPr 1731
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1430 CCAGTATATCCTCGCTGAGTTCAAGGTACGGATGCCGGATGGGCAGT 1479
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1731 oGlnTyrrileLeuArgGluPheLysValThrAspAlaArgAspGlyGlnS 1748
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1480 CRAAGCAATCCGGCATTCCTCCAGTTCACAGACTGCCAGAGCAGGCGTG 1529
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1748 exArgThrValArgGlnPheGlnPheThrAspTrpProGluGlnGlyAla 1764
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1530 CCCAAGACAGCGCAGGAGTTCATTGACTTCATCGGGCAGGTGCATAGAC 1579
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1765 ProLysSerGlyGluGlyPheIleAspPheIleGlyGlnValHisLysTh 1781
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1580 CAAGGACAGTTCGGACAGGATGGGCTATCACGTCGACATGCGAGTGCCTG 1629
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1781 rLysGluGlnPheGlyGlnAspAlaProIleSerValHisCysSerAlaG 1798
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1798 lyValGlyArgThrGlyValPheIleThrLeuSerIleValLeuGluArg 1814
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1815 MetArgTyrgLuglyValValAspIlePheGlnThrValLysValLeuAr 1831
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1831 gThrGlnArgProAlaMetValGlnThrGluAspGluTyrgLnpheCysP 1848
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1848 heGlnAlaAlaLeuGluTyrgLnuSerPheAspHisTyrrAlaThr 1863
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seq_name: pirl:A48758
seq_documentation_block:
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor-linked form P1 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A48758
R:Pan, M.G.; Rim, C.; Lu, K.P.; Florio, T.; Stork, P.J.S.
J. Biol. Chem. 268, 19284-19291, 1993
A:Title: Cloning and expression of two structurally distinct receptor-linked protein-
A:Reference number: A48758; MUID:93374907
A:Accession: A48758
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1496 <FAN>
A:Cross-references: GB:L19180
A:Note: authors translated the codon TGC for residue 27 as Gly, GAG for residue 79 as
as Phe
C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homolog
ogy
C:Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; tra
F:149-209/Domain: immunoglobulin homology <IMM1>
F:246-300/Domain: immunoglobulin homology <IMM2>
F:318-405/Domain: fibronectin type III repeat homology <FN3A>
F:411-504/Domain: fibronectin type III repeat homology <FN3B>
F:509-599/Domain: fibronectin type III repeat homology <FN3C>
F:600-684/Domain: fibronectin type III repeat homology <FN3H>
F:880-1496/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F:1256-1477/Domain: protein-tyrosine-phosphatase homology <PTP2>
F:1140/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1146/Binding site: substrate phosphate (Arg) #status predicted
F:1429/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1435/Binding site: substrate phosphate (Arg) #status predicted
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alignment_scores:
Quality: 2753.50 Length: 600
Ratio: 4.805 Gaps: 4
Percent Similarity: 95.500 Percent Identity: 85.333
alignment_block:
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US-09-743-492-1 x A48758

Align seg 1/1 to: A48758 from: 1 to: 1496

[illegible]

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1201 GlyCysGlyAsnThrGluValProAlaArgSerLeuTyrThrTyrIleG 1217
980 GAAGCTGGGCCAAGTGCCCTCCAGGGAGAGTGTGACCGCCATGGAGTCG 1029
1217 nlysLeuAlaGlnValGluProGlyGluHisValThrGlyMetGluLeuG 1234
1030 AGTTCAAGTTGCTGGCCAGCTCCAGGCCACACAGTCCCGC...TTCATC 1076
1234 luPheLysArgLeuAlaLaProArg...HisThrLeuArgAspSerPhe 1249
1077 AGCGCCAACTCCCTCGCAACAAGTTCAGAACCGGTGTGTGAACATCAT 1126
1250 ThrAlaSerLeuProCysAsnLysPheLysAsnArgLeuValAsnIleLe 1266
1127 GCCTTACGAATTCACCGGTGTGTCTCCAGCCCATCGGTGGTGTGAGG 1178
1266 uProTyrGluSerSerArgValCysLeuGlnProIleAargGlyValGluG 1283
1177 GCTCTGACTACATCAATCCAGCTTCCTGGATGTTATAGACACACAAG 1226
1283 LysSerAspTyrIleAsnAlaSerPheIleAspGlyTyrArgGlnGlnLys 1299
1227 GCTTACATAGCTACACAGGGGCTCTGGCAGAGACACCCAGAGACTTCTG 1276
1300 AlaTyrIleAlaThrGlnGlyProLeuAlaGluThrThrGluAspPheTr 1316
1277 GCGCATGCTATGGGAGCAAAATCCACCATCATCGTCTATGCTGACCAGC 1326
1316 pArgAlaLeuTyrPGLuAsnAsnSerThrIleValValMetLeuThrIysL 1333
1327 TTCGGGAGATGGCGAGGAGAAATGCCACCACTACTGCCCAGCAGAGCGC 1376
1333 euArgGluMetGlyArgGluLysCysHisGlnTyrTrpProAlaGluArg 1349
1377 TCTGCTCGCTACCACTACTTGTCTTCCACCCGATGGCTAGTACAACAT 1426
1350 SerAlaArgTyrGlnTyrPheValValAspProMetAlaGluTyrAsnMe 1366
1427 GCGCCAGTATATCTCGGTGAGTTCAGGTCACGGATCCCGGATGGCG 1476
1366 tProGluTyrIleLeuArgGluPheLysValThrAspAlaArgAspGlyG 1383
1477 AGTCAAGGACATTCGGCAGTTCACAGTTCACAGACTGCCCAGACGAGGC 1526
1383 lnSerArgThrValArg.....GlnPheThrAspTyrTrpProGluGlnGly 1397
1527 GTTGGCCACAGACGGCGAGGATTCATTACATTCATCGGCAGAGTGCATAA 1576
1398 AlaProLysSerGlyGluGlyPheIleAspPheIleGlyGlnValHisLy 1414
1577 GACCAAGGACAGTGTGGACAGGATGGCCCTATCACGGTGCACATGCAGTG 1526
1414 sThrLysGluGlnPheGlyGlnAspGlyProIleSerValHisCysSerA 1431
1627 CTGGCGTGGCGCGCACCGGGGTGTTTCATCATCTCTGAGCATCGTCTCTGGAG 1676
1431 laGlyValGlyArgThrGlyValPheIleThrLeuSerIleValLeuGlu 1447
1677 GCGATCGCTATAGGGCGTGGTGCACATGTTTCAGACCGCTGAAGACCTT 1726
1448 ArgMetLArgTyrGluGlyValValAspIlePheGlnThrValLysValle 1464
1727 GCGTACACAGCGTCTGCGCATGGTGCACAGAGGACGACGATTCACGTGT 1776
1464 uArgThrGlnArgProAlaMetValGlnThrGluAspGluTyrGlnPheC 1481
1777 GCTACCGTGGCGCCTGGAGTACCTCGGCAGCTTGTGACCACTATGCAACG 1826

1481 ysPheGlnAlaLeuGlu...LeuGlySerPheAspHisTyrAlaThr 1496

seq_name: pir2:S53089

seq_documentation_block:

protein-tyrosine-phosphatase (EC 3.1.3.48) ANLAR - African malaria mosquito (fragment)

N:Alternate names: leukocyte antigen-related protein

C:Species: Anopheles gambiae (African malaria mosquito)

C>Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000

C:Accession: S53089

R:Spilers, S.

submitted to the EMBL Data Library, March 1995

A:Description: Anlar-a transmembrane, receptor-like protein tyrosine phosphatase from th

A:Reference number: S53089

A:Accession: S53089

A:Molecule type: DNA

A:Residues: 1-1231 <SPI>

A:Cross-references: EMBL:X85217; NID:g732549; PIDN:CAA59483.1; PID:g732550

C:Genetics:

A:Introns: 1026/3; 1070/3; 1209/3

A:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;

ogy

C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane

F:208-293/Domain: fibronectin type III repeat homology <3FR>

F:619-1231/Domain: leukocyte common antigen cytosolic domain homology <LAC>

F:988-1211/Domain: protein-tyrosine-phosphatase homology <PTP>

F:872/Active site: Cys (phosphocysteine intermediate) #status predicted

F:1163/Active site: Cys (phosphocysteine intermediate) #status predicted

F:1169/Binding site: substrate phosphate (Arg) #status predicted

alignment_scores:

Quality: 2509.00 Length: 597

Ratio: 4.562 Gaps: 0

Percent Similarity: 92.127 Percent Identity: 75.042

alignment_block:

US-09-743-492-1 x S53089 ..

Align seg 1/1 to: S53089 from: 1 to: 1231

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86 AGACCAACCACCATCCCATCACCACCTGGCGGACACATCGAGCGC 135
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651 eSerHisProProIleSerIleAlaGluLeuProAsnHisValGluProL 668
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136 TCAAGCCCAACAGTGGCCCTCAAGTTCTCCAGGAGTATGAGTCCATCGAC 185
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668 euLysAlaAsnAspAsnLeuLysPheSerGlnGluTyrGluSerIleGlu 684
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186 CTGGACACAGTTCACGTGGGAGATTCAAACCTGGAGGTGAACAAGCC 235
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685 ProGlyGlnPheThrTrpAspHisSerAsnMetGluValAsnLyspr 701
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236 CAAGAACCCGCTATGGAATGTATCGCTACGACCACTCTCGAGTCATCC 285
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735 CysAspGlyTyrArgLysHisAsnAlaTyrValAlaThrGlnGlyProLe 751
   : : : : : : : : : : : : : : : : : : : : : : : : :
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751 uGlnGluThrPheGlyAspPheTrpArgMetCysTrpGluLeuLysSerS 768
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1068 eGLyArgGluLysCysPheGlnTyrTrpProHisGluArgSerValArg 1084
1386 TACCAGTACTTTGTTGACCCGATGGCTGAGTCAACATCCCCAGTA 1435
1085 TyrGlnCysTyrValValAspProIleAlaGluTyrAsnMetProGlnTyr 1101
1436 TATCTCGCTGAGTTCAGGTCACGGATCCCGGGATGGCGAGTCAAGA 1485
1101 rLysLeuArgGluPheLysValThrAspAlaArgspGlySerArgT 1118
1486 CAATCCGGCAGTTCAGTTCACAGACTGCCAGAGCAGCGCTGCCAAG 1535
1118 hrValArgGlnPheGlnPheIleThrTrpProGluGlnGlyValProLys 1134
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1135 SerGlyGlnGlyPheIleAspPheIleGlyGlnValHisLysThrLysG 1151
1586 GCAGTTTGGACAGGATGGCCCTATCACGGTGCACCTGCAGTCTGGCGTGG 1635
1151 uGlnPheGlyGlnAspGlyProIleThrValHisCysSerAlaGlyValG 1168
1636 GCCGACCCGGGTGTTCATCACTCTGAGCATGCTCTGAGCGCATGCGC 1685
1168 LyrGThrGlyValPheIleThrLeuSerIleValLeuGluArgMetGln 1184
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1185 TyrGluGlyValLeuAspValPheGlnThrValArgIleLeuArgSerG 1201
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1201 nArgProAlaMetValGlnThrGluAspGlnTyrGlnPheCysTyrArgA 1218
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seq_name: piri:TDFFLK

seq_documentation_block:
protein-tyrosine-phosphatase (EC 3.1.3.48) DLAR precursor - fruit fly (Drosophila melanogaster)
N:Alternate names: leukocyte antigen-related protein
C:Species: Drosophila melanogaster
C:Date: 14-Dec-1990 #sequence_revision 02-May-1994 #text_change 22-Jun-1999
C:Accession: A36182
R:Streuli, M.; Krueger, N.X.; Tsai, A.Y.M.; Saito, H.
Proc. Natl. Acad. Sci. U.S.A. 86, 8698-8702, 1989
Title: A family of receptor-linked protein tyrosine phosphatases in humans and Drosophila
Reference number: A36182; MUID:90046860

A:Accession: A36182
A:Molecule type: mRNA
A:Residues: 1-2029 <STR>
A:Cross-references: GB:M27700; NID:g157811; PIDN:AAA28668.1; PID:g157812
C:Genetics:
A:Gene: FlyBase: Lar
A:Cross-references: FlyBase:FBgn0000464
C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology; ogy
C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane
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F:33-2029/Product: leukocyte antigen-related protein #status predicted <MAT>
F:33-1377/Domain: extracellular #status predicted <EXT>
F:50-113/Domain: immunoglobulin homology <IMM1>
F:154-211/Domain: immunoglobulin homology <IMM2>
F:249-303/Domain: immunoglobulin homology <IMM3>
F:321-401/Domain: fibronectin type III repeat homology <FN3A>
F:416-502/Domain: fibronectin type III repeat homology <FN3B>
F:514-599/Domain: fibronectin type III repeat homology <FN3C>
F:610-699/Domain: fibronectin type III repeat homology <FN3D>
F:708-802/Domain: fibronectin type III repeat homology <FN3E>
F:811-896/Domain: fibronectin type III repeat homology <FN3F>

F:909-993/Domain: fibronectin type III repeat homology <FN3G>
F:1006-1091/Domain: fibronectin type III repeat homology <FN3H>
F:1101-1198/Domain: fibronectin type III repeat homology <FN3I>
F:1378-1402/Domain: transmembrane #status predicted <TM>
F:1403-2029/Domain: intracellular #status predicted <INT>
F:1417-2029/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F:1497-1718/Domain: protein-tyrosine-phosphatase homology <PTP1>
F:1786-2009/Domain: protein-tyrosine-phosphatase homology <PTP2>
F:51-111,161-209,256-301/Dissulfide bonds: #status predicted
F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:1670/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1676/Binding site: substrate phosphate (Arg) #status predicted
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F:1967/Binding site: substrate phosphate (Arg) #status predicted

alignment_scores:
Quality: 2503.00 Length: 595
Ratio: 4.576 Gaps: 0
Percent Similarity: 91.933 Percent Identity: 75.126
alignment_block:
US-09-743-492-1 x TDFFLK ..
Align seg 1/1 to: TDFFLK from: 1 to: 2029

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1433 SerAspProValAspMetArgArgLeuAsnPheGlnThrProGlyMetI 1449
86 AGACACCCACCCATCCCATCCAGCCATCGCGGACAAACATCGAGCGCC 135
1449 eserHisProProlleProIleSerGluPheAlaAsnHisIleGluArgL 1466
136 TCAAGCCCAACGATGCCCTCAAGTTCTCCAGAGTATGAGTCCATCGAC 185
1466 euLysSerAsnAspAsnGlnLysPheSerGlnGluTyrGluSerIleGlu 1482
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1483 ProGlyGlnGlnPheThrTrpAspAsnSerAsnLeuGluHisAsnLysSe 1499
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1499 rLysAsnArgTyrAlaAsnValThrAlaTyrAspHisSerArgValGlnL 1516
286 TTAACCTCTATCGATGGCTGCCCGGAGTGACTACATCAATGCCAATAC 335
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386 GCCCGACGACATGGCGATTTCTGGGAATGTGTGGGAACAGCGACGCG 435
1549 uGlnGluThrPheValAspPheTrpArgMetCysTrpGluLeuLysThrA 1566
436 CCACGTGTGTCTATGATGACACCGCTGGAGGAGAGTCCCGGGTAAATGT 485
1566 laThrIleValMetMetThrArgLeuGluGluArgThrArgIleLysCys 1582
486 GATCAGTACTGGCCAGCCGCTGGCACCAGACCTGTGGCTTATTCAGGT 535
1583 AspGlnTyrTrpProThrArgGlyThrGluThrTyrGlyGlnIlePheVa 1599
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1599 ThrIleThrGluThrGlnGluLeuAlaThrTyrSerIleArgThrPheG 1616
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1616 InLeuCysArgGlnGlyPheAsnAspArgGluIleLysGlnLeuGln 1632

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1783 LeuProCysAsnLysHisLysAsnArgLeuValHisIleLeuProTyrgL 1799
1136 ATTGACCCGTGTGTCTGACGCCCATCCGTGTGTGGGGCTCTGACT 1185
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1186 ACATCAATGCCAGCTTCCTGGATGTTATAGACAGCAGAGGCTTACATA 1235
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1816 yValAsnAlaSerPheIleAspGlyTyArgTyArgSerAlaTyrlle 1832
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1833 AlaAlaGlnGlyProValGlnAspAlaAlaGluAspPheTrpArgMetLe 1849
1286 ATGGGAGCACAAATCCACCATCATCTCATCTGCTGACCAAGCTTCGGGAGA 1335
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1336 TGGCAGGAGGAATGCCACGACTACTGGCCACAGACGCTGCTGCTCGC 1385
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1866 etGlyArgGluLysCysPheGlnTyTrpProHisGluArgSerValArg 1882
1386 TACCAGTACTTTTGTGACCCGATGGCTGAGTACAAATGCCCCAGTA 1435
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1883 TyrGlnTyTyValValAspProIleAlaGluTyAsnMetProGlnTy 1899
1436 TATCTTGGCTGAGTTCAGGTACCGATGCCCGGATGGGCAGTCAAGGA 1485
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1899 rLysLeuArgGluPheLysValThrAspAlaArgGlySerSerArgT 1916
1485 CAATCCGGCAGTTCCAGTTCACAGACTGGCCAGACGAGGCGGTGCCCAAG 1535
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1636 GCGCGCACCGGGGTGTTTCATCCTGACATCTGAGCATGCTCTGGAGCGCATCGCG 1685
|||||
1966 lyArgSerGlyValPheIleThrLeuSerIleValLeuGluArgMetGln 1982
1686 TATGAGGCGCTGTCGACATGTTTTCAGACCTGAAGACCTGCGGTACACA 1735
|||||
1983 TyrGluGlyValLeuAspValPheGlnThrValArgIleLeuArgSerGL 1999
1736 GCTCTCTGCATGTGTCAGACAGAGACCATGATCATGCTGTGTCACCGTG 1785
|||||
1999 nArgProAlaMetValGlnThrGluAspGlnTyHisPheCysTyArgA 2016
1786 CGGCCCTGGAGTACCTCGCGAGCTTTGACCATAT 1820
|||||
2016 laAlaLeuGluTyrlleGlySerPheAspAsnTy 2027

seq_name: pir2:T31093

seq_documentation_block:
probable protein-tyrosine-phosphatase (EC 3.1.3.48) - medicinal leech
N:Alternate names: receptor tyrosine phosphatase
C:Species: Hirudo medicinalis (medicinal leech)
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000
C:Accession: T31093
R:Gershon, T.R.; Baker, M.; Nitabach, M.; Wu, P.; Macagno, E.R.
submitted to the EMBL Data Library, December 1997
A:Description: Two receptor tyrosine phosphatases expressed by neurons and muscle cell
A:Reference number: Z20976
A:Accession: T31093
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-1437 <GER>
A:Cross-references: EMBL:AF017084; NID:g2695656; PID:g2695657; PIDN:AAB91461.1
C:Genetics:
A:Gene: LARI
C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homolog
C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembra

alignment_scores:
Quality: 2450.50 Length: 608
Ratio: 4.472 Gaps: 3
Percent Similarity: 90.132 Percent Identity: 74.342

alignment_block:
US-09-743-492-1 x T31093 ..
Align seg 1/1 to: T31093 from: 1 to: 1437

21 TTCTGCGCCACTCTCTGACCTGTGGAGATGCGGAGCTCAACTACCA 70
|||||
831 LeuSerIleHisProThrAspProVal.....ArgArgLeuGlnTyrgL 845
71 GACCCAGGTATGCGAGACACCCATCCCATCCACGACCTGCGCG 120
|||||
845 nThrGlnAlaMetAlaCysHisProSerIleProIleSerGluPheAla 862
121 ACAACATCGAGCGCTCAAGCCCAAGCAGATGGCTCAAGTTCCTCCAGGAG 170
|||||
862 laHisValGluGlnLeuLysAlaCysAsnGlyAlaArgPheSerGlnGlu 878
171 TATGAGTCCATCGACCTGGACAGCAGTTCACCTGGGAGAAATTCAAACCT 220
|||||
879 TyrGluSerIleGluProGlyGlnGlnPheThrTrpGluAlaSerSerLe 895
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221 GGAGGTGAACAGCCCAAGACCGCTATCGGATGTCATCGCTACGACC 270
1195 nileuProTyrGluSerArgValThrLeuGlnLeuIleArgGlyV 1212
1171 TGAGGGCTCTGACTACATCAATCCAGCTTCTGATGTTATAGACAG 1220
1212 aIAspGlySerAspTyrIleAsnAlaAsnPheIleAspGlyTyrArgTyr 1228
1221 CAGAAGCCCTACATAGCTACACAGGGCCCTCTGGCAGACGACCGAGGA 1270
1229 LysLysAlaTyrIleAlaThrGlnGlyProLeuAlaSerThrThrGluAs 1245
1271 CTTCCTGGCCATGCTATGGAGCACAATCCACCATCATCGTCTCATGTA 1320
1245 pPheTyrArgMetLeuTyrPheHisAsnSerThrIleValValMetLeuV 1262
1321 CCAAGCTTCGGGAGATGGCAGGAGAAATGCCACGACTACTGGCCAGCA 1370
1262 aLLysLeuArgGluMetGlyArgGluLysCysLeuGlnTyrTrpProSer 1278
1371 GAGCGCTCTGCTCGCTACAGTACTTGTGTGACCCGATGGCTGAGTA 1420
1279 GluArgSerAlaArgTyrGlnTyrPheValValAspProMetValGluTy 1295
1421 CAACATGCCCCAGTATATCTGCTGAGTTCAGGTCACGGATCACGGATG 1470
1295 rAsnMetProGlnTyrIleLeuArgGluPheLysValThrAspAlaArgA 1312
1471 ATGGCGAGTCAAGGACAATCCCGCAGTTCACAGTTCACAGACTGGCCAG 1520
1312 spGlyGlnSerArgThrIleArgGlnPheGlnPheThrAspTrpProGlu 1328
1521 CAGGGCGTCCCAAGACAGCGGAGGATTCATGTGACTTTCATCGGGCAGGT 1570
1329 GlnGlyValProLysSerGlyGluGlyPheValAspPheIleGlyGlnVa 1345
1571 GCATAAGACCAAGGACAGTTCGACAGGATGGGCTATCACGGTGCAC 1620
1345 lHisLysThrLysGluGlnPheGlyGlnAspGlyProIleThrValHisC 1362
1621 GCAGTCTGCGTGGCCCGCCAGCGGGTGTTCATCATCTGACATCGTC 1670
1362 ySgLYAlaGlyValSerArgThrGlyValPheIleAlaLeuSerValVal 1378
1671 CTGCGCGCATCGCTATGAGGGCGTGGTGCACATGTTTCAGACCGTGAA 1720
1379 LeuGluArgMetArgTyrGluGlyValValAspLeuPheGlnThrValAr 1395
1721 GACCCCTGCTACACAGCGTCCCTGCC.....ATGGTGC 1752
1395 gLeuLeuArgThrGlnArgProCysValLysLeuArgLeuGlnValG 1412
1753 AGACA...GAGGACCATCATCATCTGCTACCGTGGCCGCTGGAGTAC 1799
1412 lNThrProGluAspHisTyrAlaPheCysTyrArgAlaAlaLeuGluTyr 1428
1800 CTGCGCAGCTTTGACCACTATGCA 1823
1429 LeuGlySerPheArgHisTyrAla 1436
seq_name: pir2:T30938

seq_documentation_block:

receptor tyrosine phosphatase - medicinal leech
C:Species: Hirudo medicinalis (medicinal leech)

C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000

C:Accession: T30938

R:Gershon, T.R.; Baker, M.; Nitabach, M.; Wu, P.; Macagno, E.R.

submitted to the EMBL Data Library, December 1997

A:Description: Two receptor tyrosine phosphatases of the LAR subfamily are expressed
A:Reference number: 220939

A:Accession: T30938

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
A:Residues: 1-2051 <GER>
A:Cross-references: EMBL:AF017083; NID:G3695654; PID:G3695655; PIDN:AAB91460.1
C:Genetics:
A:Gene: LAR2
C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology; cgy

1654 rGlyValProGluHisAlaAlaProLeuLeuLeuPheHisGluGluGlyG 1671

706 AGGCTGTCAACCCCTAGACGACGAGGCCATGTGGTGCACCTGACGAGCG 755

1671 InValHisAspProAspSerGlyProIleValValHisCysSerAla 1687

756 GCGTGGCCGACCCGCTGCTTCATCGTATTGATGCCATGTGGAGCG 805

1688 GlyValGlyArgThrGlyValPheValLeuAspSerMetLeuGluAr 1704

806 GATGAAGACGAGACAGCGTGGACATCTATGGCCACGTCGACCTGCATGC 855

1704 gtleYsHisThrGlySerValAspIleTyGlyHisValThrCysLeuA 1721

856 GATCACAGGAACATACATGTGTGAGAGGAGGACACAGTACGTGTTCATC 905

1721 rGlaGlnArgAsnTyrMetValGlnThrGluAspGlnTyrIlePheIle 1737

906 CATGAGGCGCTGCTGGAGGCTGCCACGTGGCGCCACACAGAGTGCCTGC 955

1738 HisAlaAlaIleLeuGluAlaValThrSerGlyAsnThrGluValProAl 1754

956 CGCAACCTGTATGCCACATCCAGAGCTG..... 986

1754 aArgAsnLeuPheAlaHisMetGlnLysLeuLeuGluProLeuThrIleT 1771

987 ..GGCCAACTGCCTCCAGGGAGAGTGTGACCGCATCGAGCTCGAGTTC 1034

1771 hrSerGlnSerGlyHisSerThrThrIleThrGlyIleGluAlaGluPhe 1787

1035 AAGTGTGCGCCAGCTCCAAGGCCACACAGTCCCGCTTCATCAGCGCAA 1084

1788 LysLysLeuSerSerGlyLysThrSerLeuSerSerPheAlaSerAlaAs 1804

1085 CTGCGCTGCCAACAGTTCAAGACCGGCTGGTGAACATCATGCCCTACG 1134

1804 nLeuSerCysAsnLysGlnLysAsnArgLeuValAsnValLeuProTyrG 1821

1135 AATTCAACCGTGTGTCTGTCGACGCCATCCGCTGGTGGAGGGCTCTGAC 1184

1821 luThrThrArgValCysLeuGlnProIleArgGlyValAspGlySerAsp 1837

1185 TACATCAATGCCAGCTTCCTGGATGGTTATAGACAGCAGAAAGCGCTACAT 1234

1838 TyrIleAsnAlaSerPheIleAspGlyTyrArgTyrArgAlaTyrIl 1854

1235 AGCTACACAGGGCCTCTGGCAGAGACACCGAGGACTTCTGGCGCATGC 1284

1854 eAlaThrGlnGlyProLeuProAspThrValGluAspPheTrpArgAlaL 1871

1285 TATGGAGCAAAATPCCACCATCATCGTCATGCTGCACCAAGCTTCGGGAG 1334

1871 euTrpGluSerAsnCysAsnIleIleValMetLeuThrLysLeuArgGlu 1887

1335 ATGGCAGGGAGAAATGCCACCATCTATGGCCACGACGAGCGCTCTGCTGC 1384

1888 MetGlyArgGluMetCysHisGlnTyrTrpProSerGluArgSerAlaAr 1904

1385 CTACCAGTACTTGTGTGTGACCGCATGGCTGAGTCAACATGCCCCAGT 1434

1904 gTyrGlnTyrPheValValAspProLeuAlaGluTyrAsnMetProGlnT 1921

1435 ATATCCTCGGTGAGTTCAAAGTTCACGGATGCCGGATGGCAGTCAAGG 1484

1921 yIleLeuArgGluPheLysValThrAspAlaArgAspGlyGlnSerArg 1937

1485 ACAATTCGGCAGTTCCTCAGTTCCACAGCTGGCCAGCAGCGCGTGCCTCAA 1534

1938 ThrMetArgGlnPheGlnLeuThrAspTrpProGluGlnGlyValProse 1954

1535 GACAGCGCAGGGATTCACTGACTTCATCGGCGCAGGTGCATAAGACCAAG 1584

1954 rThrGlyAspGlyPheIleAspPheIleGlyGlnThrHisLysTyrLysG 1971

1585 AGCATTTGGACAGGATGGCCCTATACACGGTGCACCTGACGTGCTGGCGTG 1634
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1971 luGlnPheGlyGlnGluGlyProIleAlaValHisCysSerAlaGlyVal 1987
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1635 GCGCCACACGGGGTTCATCACTCTGAGCATCGCTCGCTGGAGCGATGGG 1684
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1988 GlyArgThrGlyValPheIleThrLeuSerIleValLeuGluArgMetAr 2004
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1685 CPTATGAGGCGTGGTGGCATGTTTCAGACCTGAGACCCCTGCGTACAC 1734
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
2004 gPheGluGlyAlaValAspValPheGlnThrValAsnValLeuArgThrG 2021
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1735 ACGTCCCTGCCATGCTGCAGACAGAGGACCATATCAGCTGCTACCGT 1784
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
2021 InArgProGlyMetValGlnThrGluGluGlnThrAlaPheCysTyrArg 2037
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1785 GCGGCGCTGGAGTACTCGGCCAGCTTTGACCACTAT 1820
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
2038 AlaAlaLeuGluTyrLeuGlySerPheAspHisTyr 2049

name: pir2:156540

seq_documentation_block:

C:protein-tyrosine-phosphatase (EC 3.1.3.48) ctp1 - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 23-Jul-1999

C:Accession: 156540

R:Sahin, M.; Hockfield, S.

J. Neurosci. 13, 4968-4978, 1993

A:Title: Protein tyrosine phosphatases expressed in the developing rat brain.

A:Reference number: 156540; MUID:94045925

A:Accession: 156540

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-398 <RES>

A:Cross-references: EMBL:U03273; NID:g414996; PID:9414997

C:Genetics:

A:Gene: ctp1

C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology; ogp

C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
F:1-157/Domain: protein-tyrosine-phosphatase homology (fragment) <ptpl>
F:225-398/Domain: protein-tyrosine-phosphatase homology (fragment) <ptp>
F:109/Active site: Cys (phosphocysteine intermediate) #status predicted
F:115/Binding site: substrate phosphate (Arg) #status predicted

alignment_scores:

Quality:	1869.00	Length:	398
Ratio:	4.893	Gaps:	0
Percent Similarity:	95.980	Percent Identity:	87.437

alignment_block:

US-09-743-492-1 x 156540 ..

Align seg 1/1 to: 156540 from: 1 to: 398

423 GAACAGCGACGGCCACTGTGTCATGATGACACGGCTGGAGGAGAAGTC 472

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1 GluGlnArgSerAlaThrValValMetThrArgLeuGluGluLys 17

473 CCGGGTAAATGTATGATCAGTACTGCCAGCCGCTGGCCAGAGACTGTG 522

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

17 rArgValLysCysAspGlnTyrTrpProAsnArgGlyThrGluThrTyrG 34

523 GCGTTATTCAGGTGACCTGTGTGGACAGTGGAGCTGGCCACATACACT 572

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

34 lPheIleGlnValThrLeuLeuAspThrMetGluLeuAlaThrPheCys 50

573 GTGCGCACTTGGCACTCCACAAAGTGGCTCCAGTGAGAGCGGTGAGCT 622

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

51 ValArgThrPheSerLeuHisLysAsnGlySerGluLysArgGluVa 67

623 GGTTCAGTTTCAGTTTCATGGCTTGGCCAGACCATGGAGTTCTCTGAGTACC 672
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
67 lArgHisPheGlnPheThrAlaTrpProAspHisGlyValProGluTyrP 84
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
673 CAATCCCATCTCTGCTTCTACGAGCGGTCAAGGCCTGCAACCCCTA 722
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
84 roThrProPheLeuAlaPheLeuArgArgValLysThrCysAsnProPro 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
723 GACGAGGCGCCATGGTGTGTCACGTGACGCGGGGGTGGCGCGCACCGG 772
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
101 AspAlaGlyProValValValHisCysSerAlaGlyValGlyArgThrGl 117
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
773 CNGCTTCATCGTATGATGTCCTGTCAGCGGGATGAAGCAGCAGAGA 822
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
117 yCysPheIleValIleGlyAlaMetLeuGluArgIleArgThrGluLysT 134
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
823 CGGTGGACATCTATGGCCACGTGACCTGCATGTCATGATGACAGAGAACTAC 872
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
134 hrValAspValTyrGlyHisValThrLeuMetArgSerGlnArgAsnTyr 150
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
873 ATGTGTCAGACGAGGACCATGTCATGTCATGTCATGAGCGCTGCTGGA 922
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
151 MetValGlnThrGluAspGlnTyrSerPheIleHisGluAlaLeuLeuGl 167
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
923 GGTGCCACGTGGCGCCACACAGAGGTGCTGCCGCCAACCTGTATGCC 972
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
167 uAlaValGlyCysGlyAsnThrGluValProAlaArgThrLeuTyrThrT 184
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
973 ACATCCAGAAGTGGCGCCAAAGTGCCTCCAGGGGAGTGTGACCGGCATG 1022
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
184 yrIleGlnLysLeuAlaGlnValGluProGlyGluHisValThrGlyMet 200
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1023 GAGCTCGAGTTCAAGTGTGTCGCGAGCTCCAGGCCACACACGTCGCGCT 1072
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
201 GluLeuGluPheLysArgLeuAlaSerLysAlaHisThrSerArgph 217
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1073 CATCAGCGCCACCTGCCCTGCAACAAGTCAAGAACCCTGGTGAACA 1122
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
217 elleThrAlaSerLeuProCysAsnLysPheLysAsnArgLeuValAsnI 234
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1123 TCATGCCCTTACGAATGACCCCTGTGTGTCAGCCCATCGCTGGTGTG 1172
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
234 leLeuProTyrGluSerArgValCysLeuGlnProIleArgGlyVal 250
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1173 GAGGCTGTGACTACATCAATGCCAGCTTCCTGGATGGTTATAGACAGA 1222
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
251 GluGlySerAspTyrIleAsnAlaSerPheIleAspGlyTyrArgGlnGl 267
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1223 GAAGGCTACATAGCTACACAGGCGCTCTGGCAGAGACCGGAGACT 1272
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
267 nLysAlaTyrIleAlaThrGlnGlyProLeuAlaGluThrThrGluAsp 284
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1273 TCTGGCGCATGCTATGGGAGCACAATTCACCATCATGCTCATGCTGACC 1322
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
284 heTrpArgAlaLeuCysGluAsnAsnSerThrIleValValMetLeuThr 300
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1323 AAGCTTCGGGAGATGGCAGGAGAAATGCCACAGTACTGCGCCAGCAGA 1372
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
301 LysLeuArgGluMetGlyArgGluLysCysHisGlnTyrTrpProAlaGl 317
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1373 GCGCTCTGCTCGCTACAGTACTTGTGTTGTTGACCCGATGGCTGAGTACA 1422
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
317 uArgSerAlaArgTyrGlnTyrPheValValAspProMetAlaGluTyrA 334
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1423 ACATGCCCCAGTATATCTCTGCTGAGTTCAGGTCAAGTCCAGGATGCCCGGAT 1472
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
334 snMetProGlnTyrIleLeuArgGluPheLysValThrAspAlaArgasp 350
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1473 GGGCAGTCAAGCAATCCGCGAGTTCAGTTCCAGACTGCCAGACAGCA 1522
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
351 GlyGlnSerArgThrValArgGlnPheGlnPheThrAspTrpProGluGl 367
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

